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☐ 1: AAA03470. cutinase...[gi:416218]

BLink, Domains, Links

LOCUS AAA03470 209 aa linear PLN 16-NOV-1993
 DEFINITION cutinase.
 ACCESSION AAA03470
 VERSION AAA03470.1 GI:416218
 DBSOURCE locus ABU03393 accession U03393.1
 KEYWORDS
 SOURCE Alternaria brassicicola
 ORGANISM Alternaria brassicicola
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria.
 REFERENCE 1 (residues 1 to 209)
 AUTHORS Yao,C. and Koeller,W.
 TITLE Cloning and characterization of a cutinase gene from Alternaria
 brassicicola
 JOURNAL Physiol. Mol. Plant Pathol.
 REFERENCE 2 (residues 1 to 209)
 AUTHORS Yao,C.
 TITLE Direct Submission
 JOURNAL Submitted (09-NOV-1993) Chenglin Yao, Plant Pathology, Cornell
 University, Geneva, NY 14456, USA
 COMMENT Method: conceptual translation.
 FEATURES
 Location/Qualifiers
 source 1..209
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 /db_xref="taxon:29001"
 Protein 1..209
 /product="cutinase"
 CDS 1..209
 /gene="cutab1"
 /coded_by="join(U03393.1:550..687,U03393.1:744..1235)"
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 61 aygasnvwvq gvggpytagl venalpagts qaaireaqrl fnlaaskcpn tpitaggysq
 121 gaavmsnaip glsaavqddi kgvvlfgytk nlqnggripn fptskttiyc etgdlvcngt
 181 liitpahllly sdeaavqapt flraqidsa
 //

Revised: August 5, 2002.

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2003-03-11 16:01

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Sequence revision history

Entrez ?

Revision History for Accession = aaa03470, Version = 1		
<i>gi</i>	<i>Version</i>	<i>Update Date</i>
<u>416218</u>	1	Nov 24 1993 5:18:45:100AM

This sequence was first seen at NCBI on Nov 17 1993 12:06:18:653AM (see Disclaimer)

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	604	60.5	209	1	CUT1_ALTBR	P41744 alternaria
2	601.5	60.2	228	1	CUT1_MAGGR	P30272 magnaporthe
3	584	58.5	224	1	CUT1_COLGL	P11373 colletotric
4	564	56.5	223	1	CUT1_ASCRA	P29292 ascochyta r
5	558.5	55.9	228	1	CUT1_COLCA	P10951 colletotric
6	558	55.9	230	1	CUT1_FUSSC	P09174 fusarium so
7	553	55.4	230	1	CUT1_FUSSO	P00590 fusarium so
8	550.5	55.1	231	1	CUT2_FUSSO	P09600 fusarium so
9	548.5	54.9	231	1	CUT3_FUSSO	P09659 fusarium so
10	445	44.5	213	1	CUT1_ASFOR	P52956 aspergillus
11	226	22.6	202	1	CUT1_BOTCI	Q00298 botrytis ci
12	197.5	19.8	217	1	CUT2_MYCTU	Q10837 mycobacteri
13	187.5	18.8	219	1	CUT2_MYCTU	Q50664 mycobacteri
14	167.5	16.8	247	1	CUT3_MYCTU	Q06318 mycobacteri
15	89	8.9	592	1	XYNB_PSEFL	P23030 pseudomonas
16	88.5	8.9	6486	1	TYCC_BACBR	Q30409 b tyrocidin
17	83	8.3	1293	1	ENFP_ECO57	Q8xbv9 escherichia
18	83	8.3	1356	1	HET1_PODAN	Q08098 podospora a
19	82	8.2	329	1	EBA3_FLAME	P36913 flavobacter
20	81	8.1	380	1	H1B1_MYCTU	Q06591 mycobacteri
21	80	8.0	466	1	GSA_SOYBN	P45621 glycine max
22	78.5	7.9	456	1	MURD_ENTFA	Q07108 enterococcu
23	78.5	7.9	481	1	GSA_LYCES	Q40147 lycopersico
24	78	7.8	377	1	HIS8_MYCLE	Q9x7b8 mycobacteri
25	78	7.8	743	1	OCT1_HUMAN	P14859 homo sapien
26	77.5	7.8	5255	1	BACA_BACLI	Q68006 b bacitraci
27	76.5	7.7	423	1	Y370_RHIME	Q52997 rhizobium m
28	76.5	7.7	453	1	GATA_CAMJE	Q9pnn2 campylobact
29	76	7.6	363	1	MURG_BACHD	Q9k9t0 bacillus ha
30	76	7.6	423	1	SYH_SALTY	Q52765 salmonella
31	76	7.6	482	1	YPT1_CABEL	P41879 caenorhabdi
32	75.5	7.6	384	1	REFC_BRUME	Q8yed7 bruceella me
33	75.5	7.6	928	1	PM11_CHLPN	Q86164 chlamydia p

Db 13 QASTTRNELETCSSDACPRITIFARGSTGTEAGNMALGVGFTFANALESAYGASNVVQGV 72

Qy 59 GGPYDAALATNLPRTGTSQANIDEKRLFALANOKCPNTPVAGYSGAALIAAASEL 118

Db 73 GGPYTAGLVENALPAGTSSAIREAQLFNLAKCPNTPITAGYSOGAAVMSNAIPGL 132

Qy 119 SGAYKEQVKGVALGYTONLQNRGGINPYPRERTKVCNVGDVCTGLTIITPAHLSYTI 178

Db 133 SAAVODQIKGVVLFYTKNLQNRGIPNFTSKTIYCTGDLVGNGLTIITPAHLLYSYD 192

Qy 179 EARGEAEARFLRDR 192

Db 193 EAAVQAPTEFLRAQI 206

RESULT 2

CUTI_MAGGR STANDARD; PRT; 228 AA.

AC P30272;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

JE Cutinase precursor (EC 3.1.1.74).

GN CUT1

OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

OX NCBI_TaxID=148305;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=4091-5-8;

RX MEDLINE=92212279; PubMed=1557023;

RA Sweigard J.A., Chumley F., Valent B.;

RT "Cloning and analysis of CUT1, a cutinase gene from Magnaporthe grisea";

RL Mol. Gen. Genet. 232:174-182(1992).

CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that penetrates the structure of plant cuticle. Allows pathogenic fungi to penetrate through the cuticular barrier into the host plant during the initial stage of the fungal infection.

CC -!- CATALYTIC ACTIVITY: Cutin + H₂O -> cutin monomers.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.

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CC -----

DR EMBL; X61500; CAA43717.1; ALT_TERM.

DR HSSP; P00390; ICDW.

DR InterPro; IPR000675; Cutinase.

DR Pfam; PF01083; Cutinase; 1.

DR PRINTS; PR00129; CUTINASE.

DR PROSITE; PS00155; CUTINASE_1; 1.

DR PROSITE; PS00931; CUTINASE_2; 1.

KW Hydrolase; Serine esterase; Signal; Glycoprotein.

FT SIGNAL 1 16

FT CHAIN 17 228

FT DISULFID 49 196

FT DISULFID 127 189

FT ACT_SITE 138 138

FT ACT_SITE 193 193

FT ACT_SITE 206 206

FT CARBOHYD 190 190

SQ SEQUENCE 228 AA; 24276 MW; BR0ACE063B9D4627 CRC64;

Query Match

Best Local Similarity 60.2%; Score 601.5; DB 1; Length 228;

Matches 117; Conservative 27; Mismatches 50; Indels 1; Gaps 1;

Qy 1 QUGATENGLESANACPDAILIFARGSTGTEAGNMALGVGFTFANALESAYGASNVVQGV 59

Db 33 QUNSVNRDLISNAACPSVILIFARASGEVGNMGLSAGTNVASRLERFRNDIWIQGVG 92

Qy 60 GPDYDAALATNLPRTGTSQANIDEKRLFALANOKCPNTPVAGYSGAALIAAASEL 119

Db 93 DYPDAAALSNFLPAGTTCGATIDEAKRMFTLANTKCPNAAVAGGYSGGTAVMNAVSEMP 152

Qy 120 GAYKEQVKGVALGYTONLQNRGGINPYPRERTKVCNVGDVCTGLTIITPAHLSYTI 179

Db 153 AAVODQIKGVVLFYTKNLQNRGIPNFTSKTIYCTGDLVGNGLTIITPAHLLYSYD 212

Qy 180 ARGEAEARFLRDR 194

Db 213 SSSAAPNWLIRQIRA 227

RESULT 3

CUTI_COLGL STANDARD; PRT; 224 AA.

AC P11373;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Cutinase precursor (EC 3.1.1.74).

GN CUTA.

OS Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella cingulata).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; Glomerella.

OX NCBI_TaxID=5457;

RN [1]

RP SEQUENCE FROM N.A.

RA Ettinger W.F., Thukral S.K., Kolattukudy P.E.;

RT "Structure of cutinase gene, cDNA, and the derived amino acid sequence from phytopathogenic fungi.";

RL Biochemistry 26:7883-7892(1987).

CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that forms the structure of plant cuticle. Allows pathogenic fungi to penetrate through the cuticular barrier into the host plant during the initial stage of the fungal infection.

CC -!- CATALYTIC ACTIVITY: Cutin + H₂O -> cutin monomers.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- INDUCTION: By contact with cutin.

CC -!- PTM: THE 2 DISULFIDE BONDS PLAY A CRITICAL ROLE IN HOLDING THE CATALYTIC RESIDUES IN JUXTA-POSITION; REDUCTION OF THE DISULFIDE BRIDGES RESULTS IN THE COMPLETE INACTIVATION OF THE ENZYME.

CC -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.

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CC -----

DR EMBL; M21443; AAA33042.1; -.

DR PIR; B27451; B27451.

DR HSSP; P00590; ICDW.

DR InterPro; IPR000675; Cutinase.

DR Pfam; PF01083; Cutinase; 1.

DR PRINTS; PR00129; CUTINASE.

DR PROSITE; PS00155; CUTINASE_1; 1.

DR PROSITE; PS00931; CUTINASE_2; 1.

KW Hydrolase; Serine esterase; Signal.

FT SIGNAL 1 16

FT CHAIN 17 224

FT DISULFID 46 194

FT DISULFID 125 187

FT ACT_SITE 136 136

POTENTIAL.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

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FT ACT_SITE 135 135 BY SIMILARITY.
FT ACT_SITE 189 189 BY SIMILARITY.
FT ACT_SITE 202 202 BY SIMILARITY.
SQ SEQUENCE 223 AA; 23520 MW; 1E82A5ADD1B5E7FB CRC64;

Query Match 56.5%; Score 564; DB 1; Length 223;
Best Local Similarity 58.6%; Pred. No. 4.7e-41;
Matches 112; Conservative 29; Mismatches 48; Indels 2; Gaps 2;

QY 5 IENLGSSANACPDATLIFARSTEGPNNGIIVGPALANGLESH-IRNIWIOGVGGPYD 63
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 34 IRSELEOGSSSPCKAILLIFARSTEGICNMGVGNPVAASALEYAGDQIIVQGVGPYT 93
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 64 AALATNPLPGTQSOANTDEKGRIFALANQKCPNTPVVGYSOGAALIAAAVSLSGAVK 123
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 94 ADLFSNPLPGTQSASAINEARVLFNEANTKPCSTPIVAGYSOGTATVMAAIPKLD-AVR 152
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 124 EOYKGVALFGYTNLQNRGIGPNYPRETRVFCNVGVDGCTGLIITPAHLSYTIARGE 183
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 153 ARVVGTVLFGYTNQNNKIKYQPDLDQYCEVDGLVCDGTLIITVSHFLYEEAAGP 212
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 184 AARFLRDRIRA 194
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 213 APEFLKSKIGA 223
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RESULT 5
CUTI_COLCA
ID CUTI_COLCA STANDARD; PRT; 228 AA.
AC PI0951;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cutinase precursor (EC 3.1.1.74).
CUA CUTA.
OS Colletotrichum capsici (Anthracnose fungus).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
OC mitosporic Phyllachoraceae; Colletotrichum.
NCBI_TaxId=5456;
[1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=ATCC 48574;
RA Ettinger W.F., Thukral S.K., Kolattukudy P.E.;
RT "Structure of cutinase gene, cDNA, and the derived amino acid
sequence from phytopathogenic fungi.";
RL Biochemistry 26:7883-7892(1987).
CC -I- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
forms the structure of plant cuticle. Allows pathogenic fungi to
penetrate through the cuticular barrier into the host plant during
the initial stage of the fungal infection.
CC -I- CATALYTIC ACTIVITY: Cutin + H ₂ O = cutin monomers.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- INDUCTION: By contact with cutin.
CC -I- PTM: THE 2 DISULFIDE BONDS PLAY A CRITICAL ROLE IN HOLDING THE
CATALYTIC RESIDUES IN JUXTA-POSITION; REDUCTION OF THE DISULFIDE
BRIDGES RESULTS IN THE COMPLETE INACTIVATION OF THE ENZYME.
CC -I- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.

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CC EMBL; M18033; AAA33043.1; .
DR PIR; A27451; A27451.
DR HSP; P00590; ICDW.
DR InterPro: IPRO00675; Cutinase.
DR Pfam; PF01083; Cutinase; 1.
DR PRINTS; PR00129; CUTINASE.

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DR PROSITE; PS00155; CUTINASE_1; 1.
DR PROSITE; PS00931; CUTINASE_2; 1.
KW Hydrolase; Serine esterase; Signal.
FT CHAIN 1 16 POTENTIAL.
FT CHAIN 17 228 CUTINASE.
FT DISULFID 49 198 BY SIMILARITY.
FT DISULFID 129 191 BY SIMILARITY.
FT ACT_SITE 140 140 BY SIMILARITY.
FT ACT_SITE 195 195 BY SIMILARITY.
FT ACT_SITE 208 208 BY SIMILARITY.
SQ SEQUENCE 228 AA; 3825D42C23DA139B CRC64;

Query Match 55.9%; Score 558.5; DB 1; Length 228;
Best Local Similarity 57.7%; Pred. No. 1.4e-40;
Matches 109; Conservative 27; Mismatches 50; Indels 3; Gaps 2;

QY 7 NGLSGSANACPDAILIFARGSTPEPGNMGITVGPALANGLESH--IRNIWQVGGPYDA 64
DB 39 NELESSSNCVKYIIFARASTPEPGNMGISAGPIVADALESRYGASQVWVQVGGPYSA 98
Y 65 ALATNF-LPRGTQANIDEKRLFPALANOKCPNTPVVGAGYSOGAALIAAAYSELGAYK 123
DB 99 DIASNIIPGTSRVAINEAKRLFTLANCKPNSAVVAGGTSQGTAYMASSISELSSTIQ 158
QY 124 EOYGVALFGYTONLQNRGGIPNYPRTKRVFCNVGDAVCTGTLLITPAHLSYTIARGE 183
DB 159 NQIKGVVLSAITNQLNIGRIPNFTSKTEVYCALADAVCYGILFILPAHFLYQDAATS 218
QY 184 AARFLRDRI 192
DB 219 APRFLAARI 227

RESULT 6
CUTL_FUSSC
ID CUTL_FUSSC STANDARD; PRT; 230 AA.
AC Q99174;
DF 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cutinase precursor (EC 3.1.1.74).
GN CUTA.
OS Fusarium solani (subsp. cucurbitae) (Nectria ipomoeae).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=57162;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PGB 153;
RA Crowhurst R.N., Binnie S.J., Bowen J.K., Hawthorne B.T., Plummer K.M.,
RT Rees-George J., Rikkerink E.H., Templeton M.D.;
RT "Effect of disruption of a cutinase gene (cuta) on virulence and
RT tissue specificity of Fusarium solani f. sp. cucurbitae race 2 toward
RT Cucurbita maxima and C. moschata.";
RL Mol. Plant Microbe Interact. 10:355-368(1997).
CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection.
CC -!- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
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CC -----
DR EMBL; U63335; AAB05922.1;

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DR HSP: P00590; 2CUT.
DR InterPro; IPR000675; Cutinase.
DR Pfam; PF01083; Cutinase; 1.
DR PRINTS; PRO0129; CUTINASE.
DR PROSITE; PS00155; CUTINASE_1; 1.
DR PROSITE; PS00931; CUTINASE_2; 1.
KW Hydrolase; Serine esterase; Glycoprotein; Signal.
FT SIGNAL 1 16 BY SIMILARITY.
FT CHAIN 17 230 CUTINASE.
FT DISULFID 47 194 BY SIMILARITY.
FT DISULFID 125 187 BY SIMILARITY.
FT ACT_SITE 136 136 BY SIMILARITY.
FT ACT_SITE 191 191 BY SIMILARITY.
FT ACT_SITE 204 204 BY SIMILARITY.
SQ SEQUENCE 230 AA; 23902 MW; 05FB3C33326405AA CRC64;

Query Match 55.9%; Score 558; DB 1; Length 230;
Best Local Similarity 55.8%; Pred. No. 1.6e-40;
Matches 110; Conservative 32; Mismatches 51; Indels 4; Gaps 3;

QY 1 QLG-AIENGLESGSANACPDAILIFARGSTPEPGNMGITVGPALANGLESHI--RNIIWQ 57
DB 30 QLGTTRDDLLNGNSACADVIFIVARGSTETGNLG-TLGPSIASNLESFCTGVDGWIQ 88
QY 58 VGGPYDAALATNFIPLRGTSQANIDEKRLFPALANOKCPNTPVVGAGYSOGAALIAAAYSE 117
DB 89 VGGAYRATLDGNALPRTSSAAIREMLGLFQOANTKCPDANTLIAGYSOGAALAAASIED 148
QY 118 LSGAVKQVKGVALFGYTONLQNRGGIPNYPRTKRVFCNVGDAVCTGTLLITPAHLSY 177
DB 149 LDSAIRDKIAGTVLFYTKNLQNRGRIPNYPADRTKVFECNVGDLVCTGSLIVAAPHLAIG 208
QY 178 IEARGEAAFLRDRI 194
DB 209 PDARGPAPEFLIEKVA 225

RESULT 7
CUTL_FUSSO
ID CUTL_FUSSO STANDARD; PRT; 230 AA.
AC P00590;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cutinase 1 precursor (EC 3.1.1.74).
GN CUTI OR CUTA.
OS Fusarium solani (subsp. pisi) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=70791;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-T-8;
RA Soliday C.L., Fluke W.H., Okita T.W., Kolattukudy P.E.;
RT "Cloning and structure determination of cDNA for cutinase, an enzyme
RT involved in fungal penetration of plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3939-3943(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89197761; PubMed=2703464;
RA Soliday C.L., Dickman M.B., Kolattukudy P.E.;
RT "Structure of the cutinase gene and detection of promoter activity in
RT the 5'-flanking region by fungal transformation.";
RL J. Bacteriol. 171:1942-1951(1989).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RX MEDLINE=92220194; PubMed=150844;
RA Martinez C., de Geus P., Lauwereys M., Matthysens G., Cambillau C.;
RT "Fusarium solani cutinase is a lipolytic enzyme with a catalytic
RT serine accessible to solvent.";
RL Nature 356:615-618(1992).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

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